

# FIG. 1

**A**

-156 CATTCTACTGTCAGTTAACCTTCATTTCTTCAC  
 120 TTTAACTTGAAGAATTAAACCAATTAAATTATATATATATAAATATAAATATAAANCTGTATCCCAGGCTGCTTATGAGAACAGCTATTAAACACAGTGGGACCCAGGA  
 1 ATGGAACCTGCTCCACACCTCTGGGTGGGGCTGACTTTGCTCTCACGGGGATCTGGCTTTGCTGCCCCGGAGTGGGTATTATCCAGGCTCTCCATTCTTTC  
 M E L L H T F C G G R W T L L L F T G I L C F V V A R G V G Y Y P R F S P F F F 40  
 121 CTTGCACTCATCGAGAACCTGAGAGATGGGAACAGAGAACAGTGTCTCATCTCTGCACCTGGGGCAACCCAGCTACTACATACCTGGCAGGAGTACCATGTCACCA  
 1 L C T H G E L E G D G E Q G E V L I S L H L A G N P S Y Y I P G Q E Y H V T I 80  
 241 TCCACTAGTACCTCTTGATGGTCTCTGGTACTGGACTTACACTCTACAGTGTCAAGGCTCAGAGCATTGGAGGCTAAAGCATTGGATTGGTATTATGAGCAGCGT  
 1 S T S A T F F D G L L V T G L Y T S T S V Q A S Q S I G G S K A F G F G I M S D R 120  
 361 CAGTTGGTACCCAGTTATGTGCACTGGTCTGGTACCTCCACAAACCTAAAGTGTATGGATTGGACCCAGCAGGAGTGTCACTTCATG  
 1 Q F G T Q F M C S V V A S H V S H L P T T N L S F V W I A P P A G T G C V N F M 160  
 481 GCCACAGCAACACATAGGGCAAGTTTCAGGATGGCTGGACAAACACTGTGGAACACAGGCTCTACTGAAGCTCTGGGGCTAATTAGCCAAATTCACAGTGA  
 1 A T A T H R G V Y I F K D A L A Q Q L C E Q G A P T E A P L R P N L A E I H S E 200  
 601 AGCATCTTTACGAGATGTTTGACTCATATAAGCTCAGGAATTGAATCCTAAAGTGAATCCTGGCTCAGTGCAGAAATTGGCAAGTGGTGGAGCTGTGGTCAATTATGCATGGGG  
 1 S I L L R D D F D S Y K L Q E L N P N I H L Q C R N C E V G E Q C G A I M H G G 240  
 721 GCACTACTTTTGTGATCCGTATGGCAAGAGAAATTGATAACTGTCAATGAAACACAACCTACGGCATCTGTTTCAGTTTCTATTGGTCAAGGATGTCAGGTTCA  
 1 A V T F C D P Y G P R E L I T V Q M N T T T A S V L Q F S I G S G S C R F S Y S 280  
 841 GACCCCTGAAATTGTGGTGTCAACAAAGATAATTCACTAGTGGATGCCATTGGAGAGAAATTAGTGTCTCTCCATGTTAGCATCATTACCTCTCTGAA  
 1 D P G I V V S Y T K N N S S S W M P L E R I S A P S N V S T I I I I Y L P P E 320  
 961 GCTAAAGGAAAATGTGAAATTCCGGGGAGGAGAACATGCAAGGAGGTGATGTGATGGCTGGGACTGGATAACATTGATTATCAATGTCATAAAGAGTC  
 1 A K G E N V K F R W R Q E N M Q A G D V Y E A C W A L D N I T I N A A H K E V 360  
 1081 GTGTTAGAAGACAATCTAGATCCAATGGACACAGGAACTGGCTTTCTGGGGCTACTGTAAAGCATACTGTGAGTGGATGAAACTCTATATATTTCATGGTACAGAAAGC  
 1 V L E D N L D P M D T G N N L F F P G A T V K H T C Q S D G N S I Y F H G T E S 400  
 1201 ATGGAATACAACCTTGTACTACAGAGATGTGGATCTTCCAGTGGAGACATCCAGGACCTGGCTGAAGAGTTGAGAATCTACCTGGGGAAATAGTGGAGCAGTAATT  
 1 S E Y N F A T T R D V D L S S E D I Q D Q H S E E F E N L P A G W E I V G A V I 440  
 1321 GGAACACAATGTGGAAACCATAGATCGGTTCATCTGTGTTGGGGCTACTGTAAAGGATGGAGAAAAGTTGCACTCTTACATGGATACCCGGATATGGAACTAAAGTTTATTT  
 1 G T E C G T I E S G S S L V F L K D G E R K V C T P Y M D T T G Y G N L R F Y F 480  
 1441 ATCATGGGGGAATGTGGAGTCCAGGAGAACTCATGAAAATGTAATTCTTATGTCAGATTGATGGTAGAAAAGAGCATATTATGGATACCTTGTATTCTATAAG  
 1 I M G G M C S P G E S H E N D V I L Y A Q I D G R K E H I T M O T L A Y S S Y K 520  
 1561 GTTACTCTCTGTTCTGTCTGTCATAAAGCTGATCTACAAACACCTGCTACTAAATTGGTGAAGGAAACCCAGTCACCGTGGCTCATAACTTAAATGTTGGGCTGTGGATTGTC  
 1 V T S L V S A Y I S P D L Q T P A T C L K F C L K Q T S H R G H N L V W A V D F V 560  
 1681 CAGTGCTACCTGTATTGGTCTCCACTGAATCACATATGGTCACTTACCTGGATGGTGGCTGCACCGCTGGAAACAGTGTGAGCTGGATGGAAATTCTACAAAATCATGG  
 1 H V L P V L P S T E S H M V Q F S I N L G G C G S H Q P G N S V S L E F S T N H G 600  
 1801 CCTAGTTGGCTTTGGTCACTGGAGTGTCTCCAGAGCTATGTGTCAGGATCTACCCAGCAG-  
 1 R S W S L L H S E C L P E L C A G S H L P H S -

**B**

1321 ATTACATTTATCACGTGAAATGCAAGAAACAGTATTATACATATTTAAAGGTCAATACAGAACCCATAATGGCAGGTTAGGGCTACCATGTAATTTAAATGTCATAA  
 1441 TGTCTAGGTGGTAAGTATTATACATGCACTGAGTTACTGATTGTTATTTACCTGGCTACAGTGGCTTACAGCTAACACAGGGCATTTTTCCAAATGGCAACATCCATTGGCG  
 1561 TCTGAGGAGAACATTGTTCTTATGGCATTTGAACCTGGCTATGAGCTGGCAGCTAAATAAACATTCTGGCTATGGGTTACCATACACACTGGTACCTCATGACATGAA  
 1681 AAATATGACTCACATTAAATCAGTAAGATCAGTCAAGTATAGTACGGTGGCTTAATCTGCCAAATAAACATTAGAATTGTTATTTATTTATTTAAAGATTGAGATTGACTCATT  
 1801 CTTGACTCTTGATCACATTGGCTAGTTATGGTCATAGACAGGCTACATACATTAGTCAAGTCAAGTGGATTCTATCCAGGAGTGGCTGGGATTTACTATCACCTGGGTTAAATGCCACTTCAATTGAA  
 1921 GTGACTGTCAAGTAATCAACATTGGCTACAGATGCACTTGGATGGCTTAAATGGCTTAAACATGTCAGGCTGGATGGCTGGGATTTAAATGCCACTTCAATTGAA  
 2041 ACTTCCAGGTACAAAAATAGAATGGACATTTAAACATGTCAGGCTTAAACATGTCAGGCTGGATGGCTGGGATTTAAATGCCACTTCAATTGAA

GGTAAATTAGTGTAGCCATGAGC  
 G \* 432

FIG.2

A

Xenopus	1:ME-LLHTFCGGRWTL	59
mouse	1:..RGCWAPRALVLA..	58
human	1:..RSGWARQTFLLA..	57
Xenopus	60:SLHLAGNPSYYIIPGQEYHVTISTSTFFDGLLVTGLYTSTS	119
mouse	59:...I...H...M.....	118
human	58:...I...H...M.....	117
Xenopus	120:RQFGIQFMCSVVAHVSHLPTTNLSFMIAAPPAGTCVNFMATATHRGQVIFKDALAQQL	179
mouse	119:H.....	178
human	118:H.....	177
Xenopus	180:CEQGAPTEAPLRPNLAEIHSESILLRDDFDSYKLQE	239
mouse	179:...TAYSH.....D.VI.....QQL.....VE.S.....T...	238
human	178:...DVTVH.H.....D.I.....HQLQ.....VE.N.....T...	237
Xenopus	240:GAVTFCDPYGPRELITVQMNITTAASVLQFSIGSGSCRFSYSDPGMYSMTTRNNSSSMPL	299
mouse	239:N.....E.....T.TCL.....S.T.....A.....TAD.IQ.	298
human	238:N.....E.....T.GL.....S.T.....A.....AD.IQ.	297
Xenopus	300:ERISAPSNSVSTIICHITLPEAKGENMKRPRQENMQADQVYEACWALDNIIINWAKE	359
mouse	299:K.R.....V...L...E.....S.Q.Q.K.DSLRV.E.....M.S.R.	358
human	298:K.R.....L...E.D.....Q.Q.K..LRV.E.....M.S.R.Q	357
Xenopus	360:IVLLEONLDPMDTGNWLFFPGATVKHITQSDGNSTYFHGTSSSYNFAITRDVDSLSEDIQ	419
mouse	359:....V.....S.....N.G.F.....T.....	418
human	358:....S.....V.....N.G.F.....T.....	417
Xenopus	420:DQWSEEEFENLPIAGIEIVGAVIGTETCGTIESGSEIUVFLRDGERRYCTPYMDTTGYGNLRFY	479
mouse	419:E.....S.Q.T.D.L.V.A.D.V.....L.....L.....S.....	478
human	418:E.....S.Q.T.DVL.....V.....L.....L.....S.....	477
Xenopus	480:PIIMGMESPGESENHDVILYACTIDGRKEHTIIMOTLAFSSYKVTSLSVASIVSPDLQTPATK	539
mouse	479:V.I.D.M.....I.K.E.....A.L.T.....P.....M.N.E.	538
human	478:V.I.D.N.....I.K.E.....T.L.S.....P.....M.N.E.	537
Xenopus	540:FCIKOTSFRGHNLNVWAVDFHVFLPVLPSTIESHMQFSINLGCQSHQPGNSVSLEFSTNR	599
mouse	539:...R.I.K.Q.M.R.....F.....M.....I.....T.....	598
human	538:...R.I.K.N.Q.I.R.....F.....M.....I.....T.....	597
Xenopus	600:GRSWSSLRHSCLCPBLKAQSPHPAS	
mouse	599:.....I.....P.....	
human	598:.....I.....P.....	

B

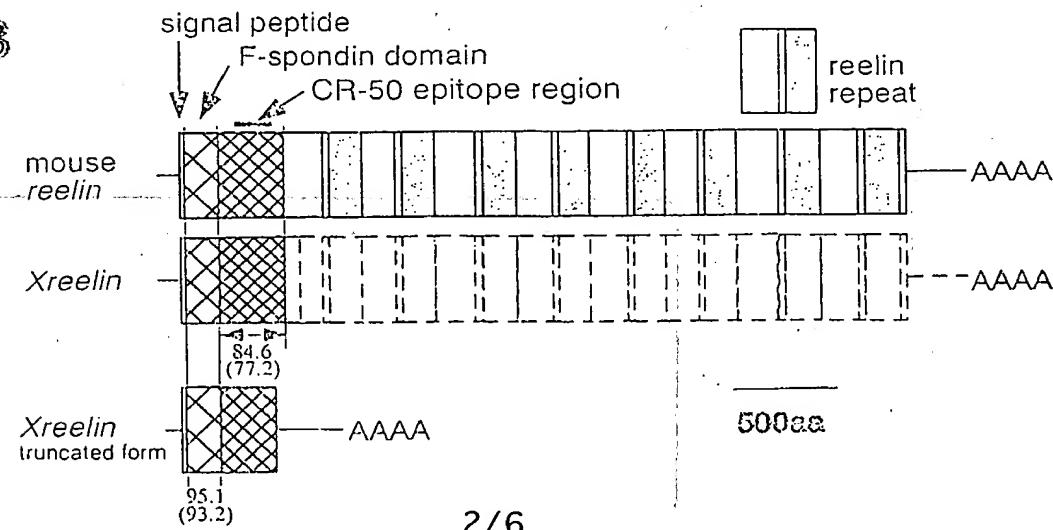


FIG.3

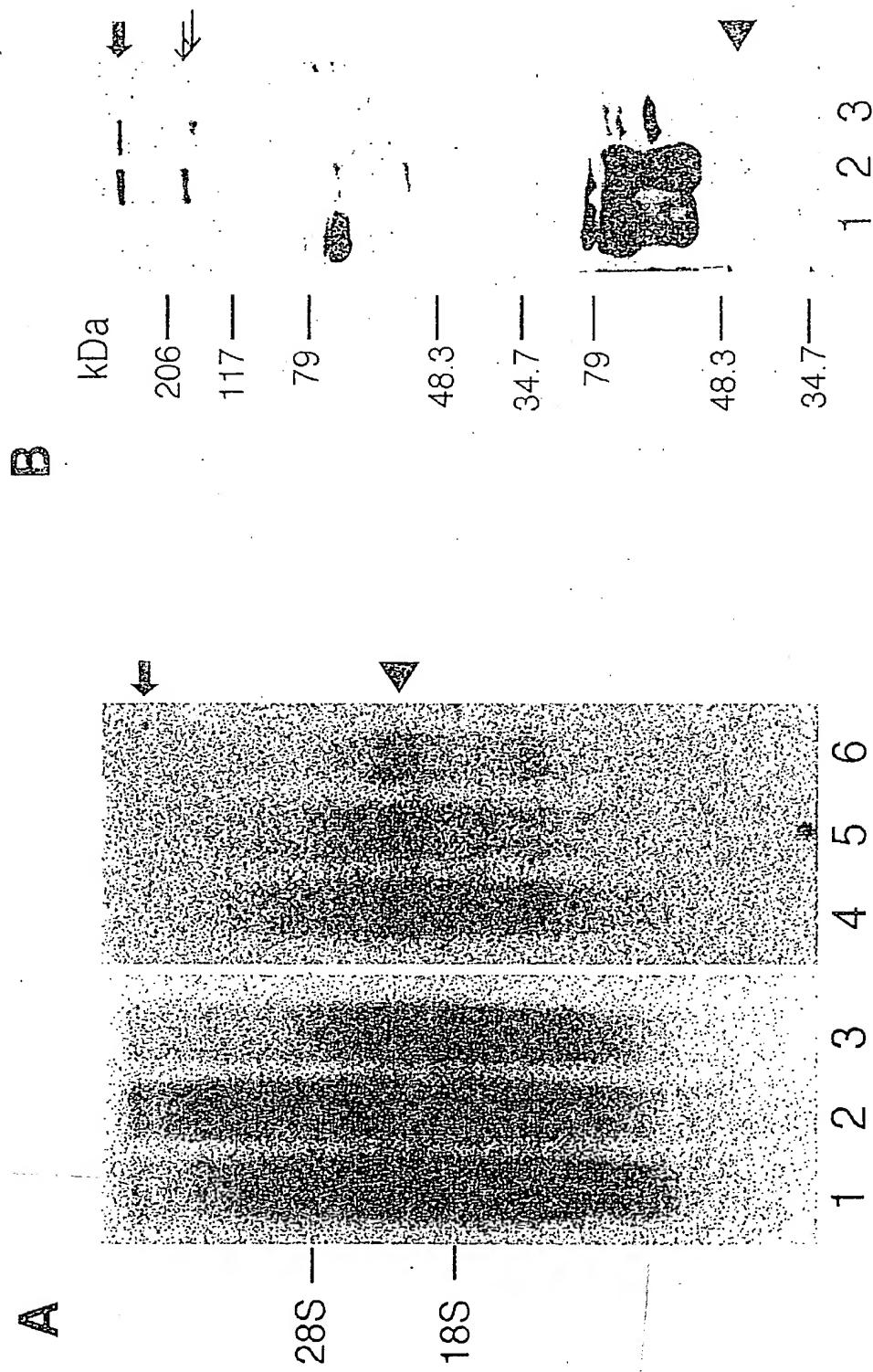


FIG.4

intact and truncated forms

truncated form

*Histon H4*

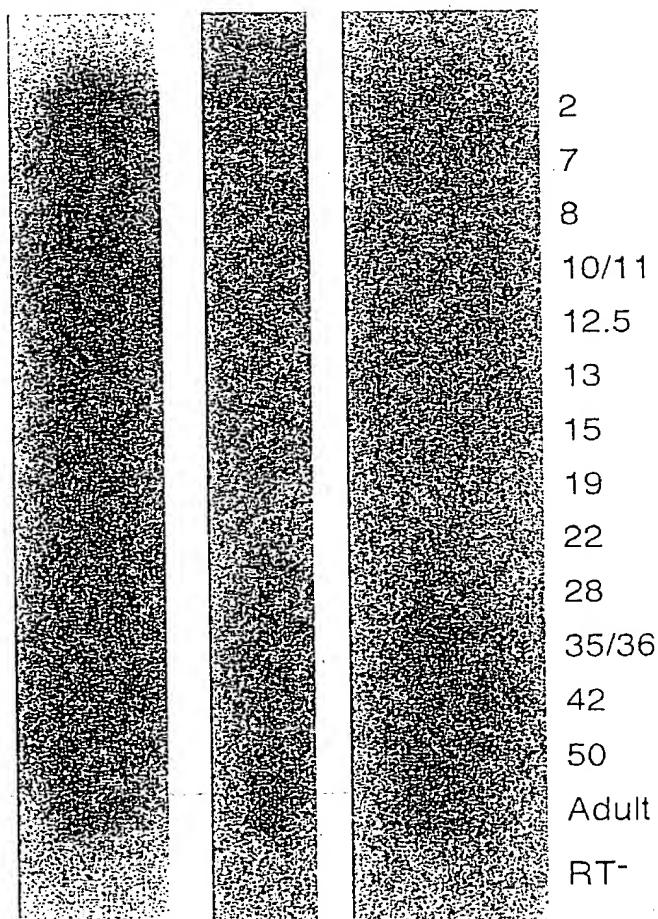


FIG.5

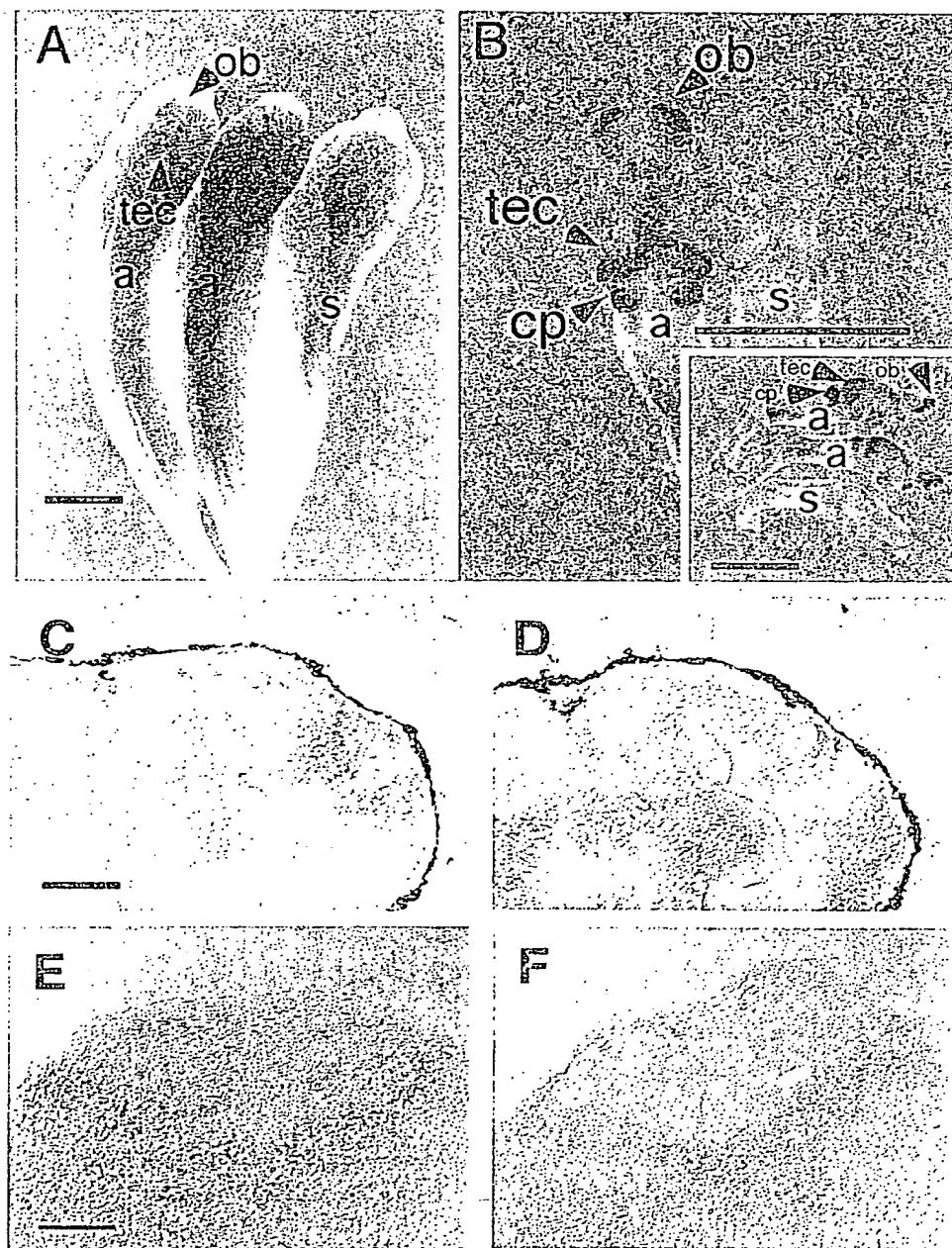


FIG.6

